



## SEQUENCE LISTING

&lt;110&gt; Lingappa, Jaisri

5 Lingappa, Vishwanath

&lt;120&gt; HIV Capsid Assembly Associated Compositions and Methods

&lt;130&gt; UCSF.002.01US

10

&lt;140&gt; US 10/040,206

&lt;141&gt; 2002-01-02

&lt;150&gt; US 60/039,309

15 &lt;151&gt; 1997-02-07

&lt;150&gt; US 09/020,144

&lt;151&gt; 1998-02-06

20 &lt;160&gt; 6

&lt;210&gt; 1

&lt;211&gt; 1610

&lt;212&gt; DNA

25 &lt;213&gt; HIV

&lt;220&gt;

&lt;223&gt; DNA coding sequence for HIV capsid protein Pr55

30 &lt;400&gt; 1

ATGGGTGCGA	GAGCGTCGGT	ATTAAGCGGG	GGAGAATTAG	ATAAATGGGA	AAAAATTCGG	60
TTAAGGCCAG	GGGGAAAGAA	AAAATATAAG	TTAAAACATA	TAGTATGGGC	AAGCAGGGAG	120
CTAGAACGAT	TCGCAGTCAA	TCCTGGCCTG	TTAGAAACAT	CAGAAGGCTG	CAGACAAATA	180
35 TTGGGACAGC	TACAGCCATC	CCTTCAGACA	GGATCAGAAG	AACTTAGATC	ATTATATAAT	240
ACAGTAGCAA	CCCTCTATTG	TGTACATCAA	AGGATAGATG	TAAAAGACAC	CAAGGAAGCT	300
TTAGAGAAGA	TAGAGGAAGA	GCAAAACAAA	AGTAAGAAAA	AGGCACAGCA	AGCAGCAGCT	360
GCAGCTGGCA	CAGGAAACAG	CAGCCAGGTC	AGCCAAAATT	ACCCTATAGT	GCAGAACCTA	420
CAGGGGCAAA	TGGTACATCA	GGCCATATCA	CCTAGAACTT	TAAATGCATG	GGTAAAAAGTA	480
40 GTAGAAGAAA	AGGCTTTCAG	CCCAGAAGTA	ATACCCATGT	TTTCAGCATT	ATCAGAAGGA	540
GCCACCCAC	AAGATTTAAA	CACCATGCTA	AACACAGTGG	GGGGACATCA	AGCAGCCATG	600

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CAAATGTAA AAGAGACTAT CAATGAGGAA GCTGCAGAAT GGGATAGAGT GCATCCAGTG 660  
 CATGCAGGGC CTATTGCACC AGGCCAAATG AGAGAACCAA GGGGAAGTGA CATAGCAGGA 720  
 ACTACTAGTA CCCTTCAGGA ACAAATAGGA TGGATGACAA ATAATCCACC TATCCCAGTA 780

5 GGAGAAATCT ATAAAAGATG GATAATCCTG GGATTAAATA AAATAGTAAG AATGTATAGC 840  
 CCTACCAGCA TTCTGGACAT AAGACAAGGA CCAAAGGAAC CCTTTAGAGA TTATGTAGAC 900  
 CGGTTCTATA AAACCTAAG AGCCGAACAA GCTTCACAGG ATGTAAAAAA TTGGATGACA 960  
 GAAACCTTGT TGGTCCAAAA TGCAAACCCA GATTGTAAGA CTATTTTAAA AGCATTGGGA 1020  
 CCAGCAGCTA CACTAGAAGA AATGATGACA GCATGTCAGG GAGTGGGGGG ACCCGGCCAT 1080  
 10 AAAGCAAGAG TTTTGGCTGA AGCCATGAGC CAAGTAACAA ATCCAGCTAA CATAATGATG 1140  
 CAGAGAGGCA ATTTTAGGAA CCAAAGAAAG ACTGTTAAGT GTTTC AATTG TGGCAAAGAA 1200  
 GGGCACATAG CCAAAAATTG CAGGGCCCCCT AGGAAAAGG GCTGTTGGAG ATGTGGAAGG 1260  
 GAAGGACACC AAATGAAAGA TTGCACTGAG AGACAGGCTA ATTTTTTAGG GAAGATCTGG 1320  
 CCTTCCTACA AGGGAAGGCC AGGGAATTTT CTTCAGAGCA GACCAGAGCC AACAGCCCCA 1380  
 15 CCAGAAGAGA GCTTCAGGTT TGGGGAGGAG AAAACAACCTC CCTCTCAGAA GCAGGAGCCG 1440  
 ATAGACAAGG AACTGTATCC TTAACTTCC CTCAGATCAC TCTTTGGCAA CGACCCCTCG 1500  
 TCACAATAAG GATAGGGGGG CAACTAAAGG AAGCTCTATT AGATACAGGA GCAGATGATA 1560  
 CAGTATTAGA AGAAATGAAT TTGCCAGGAA AATGGAAACC AAAAATGATA 1610

20 <210> 2  
 <211> 24  
 <212> PRT  
 <213> Triticum aestivum

25 <220>  
 <223> peptide fragment of host cell (wheat germ) protein HP68  
 <400> 2

30 Pro Arg Pro Tyr Leu Asp Val Lys Gln Arg Leu Lys Ala Ala Arg Val  
 1 5 10 15  
 Ile Arg Ser Leu Leu Arg Ser Asn  
 20

35 <210> 3  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

40 <220>  
 <223> Degenerate oligonucleotide C-terminal peptide sequence of WGHP68

&lt;400&gt; .3

5 ATGAATTCAC TGGGACTGCG GATAGATTAC TGGTACTGGG GATC 44

&lt;210&gt; 4

&lt;211&gt; 42

&lt;212&gt; DNA

10 &lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Degenerate oligonucleotide C-terminal peptide sequence of WGHP68

15 &lt;400&gt; 4

ATGAATTCAC TGGGCTCTGA TAGATTACTG GTACTGGGGA TC 42

&lt;210&gt; 5

20 &lt;211&gt; Length:604

&lt;212&gt; PRT

&lt;213&gt; Triticum aestivum

&lt;400&gt; 5

25

Met Ala Asp Arg Leu Thr Arg Ile Ala Ile Val Ser Glu Asp Lys Cys

1 5 10 15

Lys Pro Lys Lys Cys Arg Gln Glu Cys Lys Lys Ser Cys Pro Val Val

20 25 30

30 Lys Thr Gly Lys Leu Cys Ile Glu Val Ser Pro Val Ala Lys Leu Ala

35 40 45

Phe Ile Ser Glu Glu Leu Cys Ile Gly Cys Gly Ile Cys Val Lys Lys

50 55 60

Cys Pro Phe Asp Ala Ile Glu Ile Ile Asn Leu Pro Lys Asp Leu Glu

35 65 70 75 80

Lys Asp Thr Thr His Arg Tyr Gly Pro Asn Thr Phe Lys Leu His Arg

85 90 95

Leu Pro Val Pro Arg Pro Gly Gln Val Leu Gly Leu Val Gly Thr Asn

100 105 110

40 Gly Ile Gly Lys Ser Thr Ala Leu Lys Val Leu Ala Gly Lys Leu Lys

115 120 125

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Pro Asn Leu Gly Arg Phe Lys Asn Pro Pro Asp Trp Gln Glu Ile Leu  
 130 135 140

Thr Tyr Phe Arg Gly Ser Glu Leu Gln Asn Tyr Phe Thr Arg Ile Leu

5 145 150 155 160  
 Glu Asp Asn Leu Lys Ala Ile Ile Lys Pro Gln Tyr Val Asp His Ile  
 165 170 175  
 Pro Lys Ala Val Gln Gly Asn Val Gly Gln Val Leu Glu Gln Lys Asp  
 180 185 190

10 Glu Arg Asp Met Lys Asn Glu Leu Cys Val Asp Leu Glu Leu Asn Gln  
 195 200 205  
 Val Ile Asp Arg Asn Val Gly Asp Leu Ser Gly Gly Glu Leu Gln Arg  
 210 215 220  
 Phe Ala Ile Ala Val Val Ala Val Gln Ser Ala Glu Ile Tyr Met Phe

15 225 230 235 240  
 Asp Glu Pro Ser Ser Tyr Leu Asp Val Lys Gln Arg Leu Lys Ala Ala  
 245 250 255  
 Arg Val Ile Arg Ser Leu Leu Arg Ser Asn Ser Tyr Val Ile Val Val  
 260 265 270

20 Glu His Asp Leu Ser Val Leu Asp Tyr Leu Ser Asp Phe Ile Cys Cys  
 275 280 285  
 Leu Tyr Gly Lys Pro Gly Ala Tyr Gly Val Val Thr Leu Pro Phe Ser  
 290 295 300  
 Val Arg Glu Gly Ile Asn Ile Phe Leu Ala Gly Phe Val Pro Thr Glu

25 305 310 315 320  
 Asn Leu Arg Phe Arg Asp Glu Ser Leu Thr Phe Lys Ile Ala Glu Thr  
 325 330 335  
 Gln Glu Ser Ala Glu Glu Val Ala Thr Tyr Gln Arg Tyr Lys Tyr Pro  
 340 345 350

30 Thr Met Ser Lys Thr Gln Gly Asn Phe Lys Leu Ser Val Val Glu Gly  
 355 360 365  
 Glu Phe Thr Asp Ser Gln Ile Val Val Met Leu Gly Glu Asn Gly Thr  
 370 375 380  
 Gly Lys Thr Thr Phe Ile Arg Met Leu Ala Gly Leu Leu Lys Pro Asp

35 385 390 395 400  
 Thr Met Glu Gly Thr Glu Val Glu Ile Pro Glu Phe Asn Val Ser Tyr  
 405 410 415  
 Lys Pro Gln Lys Ile Ser Pro Lys Phe Gln His Pro Val Arg His Leu  
 420 425 430

40 Leu His Ser Lys Ile Arg Asp Ser Tyr Thr His Pro Gln Phe Val Ser  
 435 440 445

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Asp Val Met Lys Pro Leu Gln Ile Glu Gln Leu Met Asp Gln Glu Val  
450 455 460

Ile Asn Leu Ser Gly Gly Glu Leu Gln Arg Val Ala Leu Cys Leu Cys

5 465 470 475 480

Leu Gly Lys Pro Ala Asp Ile Tyr Leu Ile Asp Glu Pro Ser Ala Tyr

485 490 495

Leu Asp Ser Glu Gln Arg Ile Val Ala Ser Lys Val Ile Lys Arg Phe

500 505 510

10 Ile Leu His Ala Lys Lys Thr Ala Phe Ile Val Glu His Asp Phe Ile

515 520 525

Met Ala Thr Tyr Leu Ala Asp Lys Val Ile Val Tyr Glu Gly Leu Ala

530 535 540

Ser Ile Asp Cys Thr Ala Asn Ala Pro Gln Ser Leu Val Ser Gly Met

15 545 550 555 560

Asn Lys Phe Leu Ser His Leu Asp Ile Thr Phe Arg Arg Asp Pro Thr

565 570 575

Asn Tyr Arg Pro Arg Ile Asn Lys Leu Glu Ser Thr Lys Asp Arg Glu

580 585 590

20 Gln Lys Asn Ala Gly Ser Tyr Tyr Tyr Leu Asp Asp

595 600

<210> 6

<211> 599

25 <212> PRT

<213> Homo sapiens

<400> 6

30 Met Ala Asp Lys Leu Thr Arg Ile Ala Ile Val Asn His Asp Lys Cys

1 5 10 15

Lys Pro Lys Lys Cys Arg Gln Glu Cys Lys Lys Ser Cys Pro Val Val

20 25 30

Arg Met Gly Lys Leu Cys Ile Glu Val Thr Pro Gln Ser Lys Ile Ala

35 35 40 45

Trp Ile Ser Glu Thr Leu Cys Ile Gly Cys Gly Ile Cys Ile Lys Lys

50 55 60

Cys Pro Phe Gly Ala Leu Ser Ile Val Asn Leu Pro Ser Asn Leu Glu

65 70 75 80

40 Lys Glu Thr Thr His Arg Tyr Cys Ala Asn Ala Phe Lys Leu His Arg

85 90 95

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Leu Pro Ile Pro Arg Pro Gly Glu Val Leu Gly Leu Val Gly Thr Asn  
100 105 110  
Gly Ile Gly Lys Ser Ala Ala Leu Lys Ile Leu Ala Gly Lys Gln Lys

5 115 120 125  
Pro Asn Leu Gly Lys Tyr Asp Asp Pro Pro Asp Trp Gln Glu Ile Leu  
130 135 140  
Thr Tyr Phe Arg Gly Ser Glu Leu Gln Asn Tyr Phe Thr Lys Ile Leu  
145 150 155 160

10 Glu Asp Asp Leu Lys Ala Ile Ile Lys Pro Gln Tyr Val Ala Arg Phe  
165 170 175  
Leu Arg Leu Ala Lys Gly Thr Val Gly Ser Ile Leu Asp Arg Lys Asp  
180 185 190  
Glu Thr Lys Thr Gln Ala Ile Val Cys Gln Gln Leu Asp Leu Thr His

15 195 200 205  
Leu Lys Glu Arg Asn Val Glu Asp Leu Ser Gly Gly Glu Leu Gln Arg  
210 215 220  
Phe Ala Cys Ala Val Val Cys Ile Gln Lys Ala Asp Ile Phe Met Phe  
225 230 235 240

20 Asp Glu Pro Ser Ser Tyr Leu Asp Val Lys Gln Arg Leu Lys Ala Ala  
245 250 255  
Ile Thr Ile Arg Ser Leu Ile Asn Pro Asp Arg Tyr Ile Ile Val Val  
260 265 270  
Glu His Asp Leu Ser Val Leu Asp Tyr Leu Ser Asp Phe Ile Cys Cys

25 275 280 285  
Leu Tyr Gly Val Pro Ser Ala Tyr Gly Val Val Thr Met Pro Phe Ser  
290 295 300  
Val Arg Glu Gly Ile Asn Ile Phe Leu Asp Gly Tyr Val Pro Thr Glu  
305 310 315 320

30 Asn Leu Arg Phe Arg Asp Ala Ser Leu Val Phe Lys Val Ala Glu Thr  
325 330 335  
Ala Asn Glu Glu Glu Val Lys Lys Met Cys Met Tyr Lys Tyr Pro Gly  
340 345 350  
Met Lys Lys Lys Met Gly Glu Phe Glu Leu Ala Ile Val Ala Gly Glu

35 355 360 365  
Phe Thr Asp Ser Glu Ile Met Val Met Leu Gly Glu Asn Gly Thr Gly  
370 375 380  
Lys Thr Thr Phe Ile Arg Met Leu Ala Gly Arg Leu Lys Pro Asp Glu  
385 390 395 400

40 Gly Gly Glu Val Pro Val Leu Asn Val Ser Tyr Lys Pro Gln Lys Ile  
405 410 415

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Ser Pro Lys Ser Thr Gly Ser Val Arg Gln Leu Leu His Glu Lys Ile  
420 425 430

Arg Asp Ala Tyr Thr His Pro Gln Phe Val Thr Asp Val Met Lys Pro

5 435 440 445

Leu Gln Ile Glu Asn Ile Ile Asp Gln Glu Val Gln Thr Leu Ser Gly  
450 455 460

Gly Glu Leu Gln Arg Val Arg Leu Arg Leu Cys Leu Gly Lys Pro Ala  
465 470 475 480

10 Asp Val Tyr Leu Ile Asp Glu Pro Ser Ala Tyr Leu Asp Ser Glu Gln  
485 490 495

Arg Leu Met Ala Ala Arg Val Val Lys Arg Phe Ile Leu His Ala Lys  
500 505 510

Lys Thr Ala Phe Val Val Glu His Asp Phe Ile Met Ala Thr Tyr Leu

15 515 520 525

Ala Asp Arg Val Ile Val Phe Asp Gly Val Pro Ser Lys Asn Thr Val  
530 535 540

Ala Asn Ser Pro Gln Thr Leu Leu Ala Gly Met Asn Lys Phe Leu Ser  
545 550 555 560

a 20 Gln Leu Glu Ile Thr Phe Arg Arg Asp Pro Asn Asn Tyr Arg Pro Arg  
565 570 575

Ile Asn Lys Leu Asn Ser Ile Lys Asp Val Glu Gln Lys Lys Ser Gly  
580 585 590

Asn Tyr Phe Phe Leu Asp Asp

25 595

30

35

40